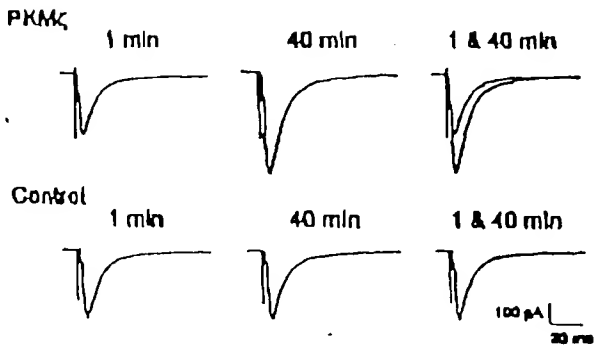

FIGURE 1A

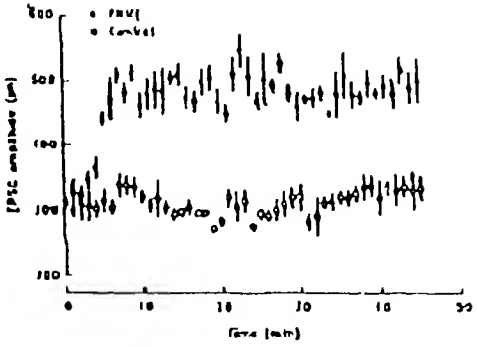

FIGURE 1B

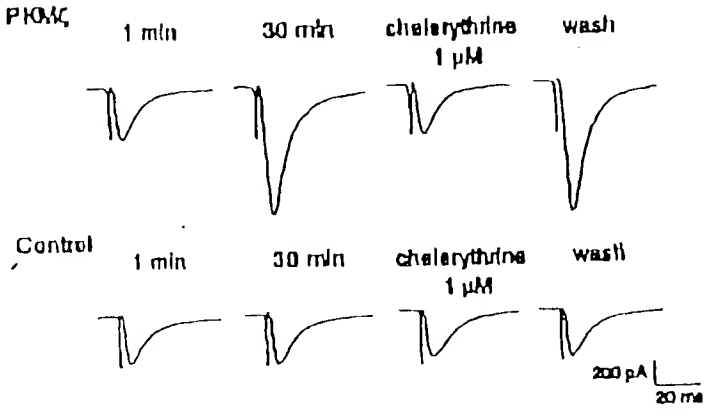

FIGURE 2A

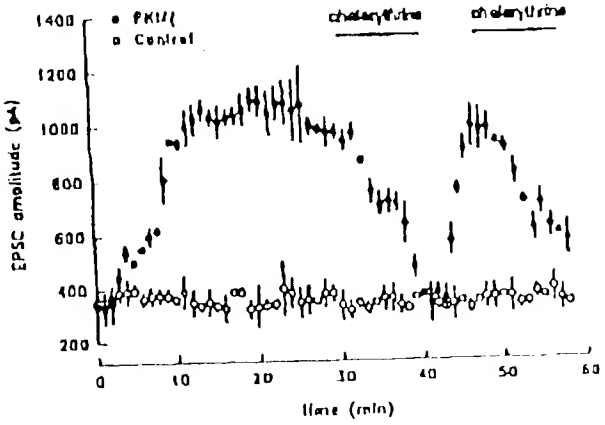

FIGURE 2B

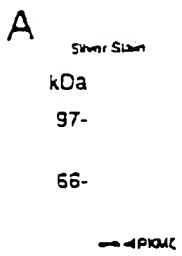

FIGURE 3

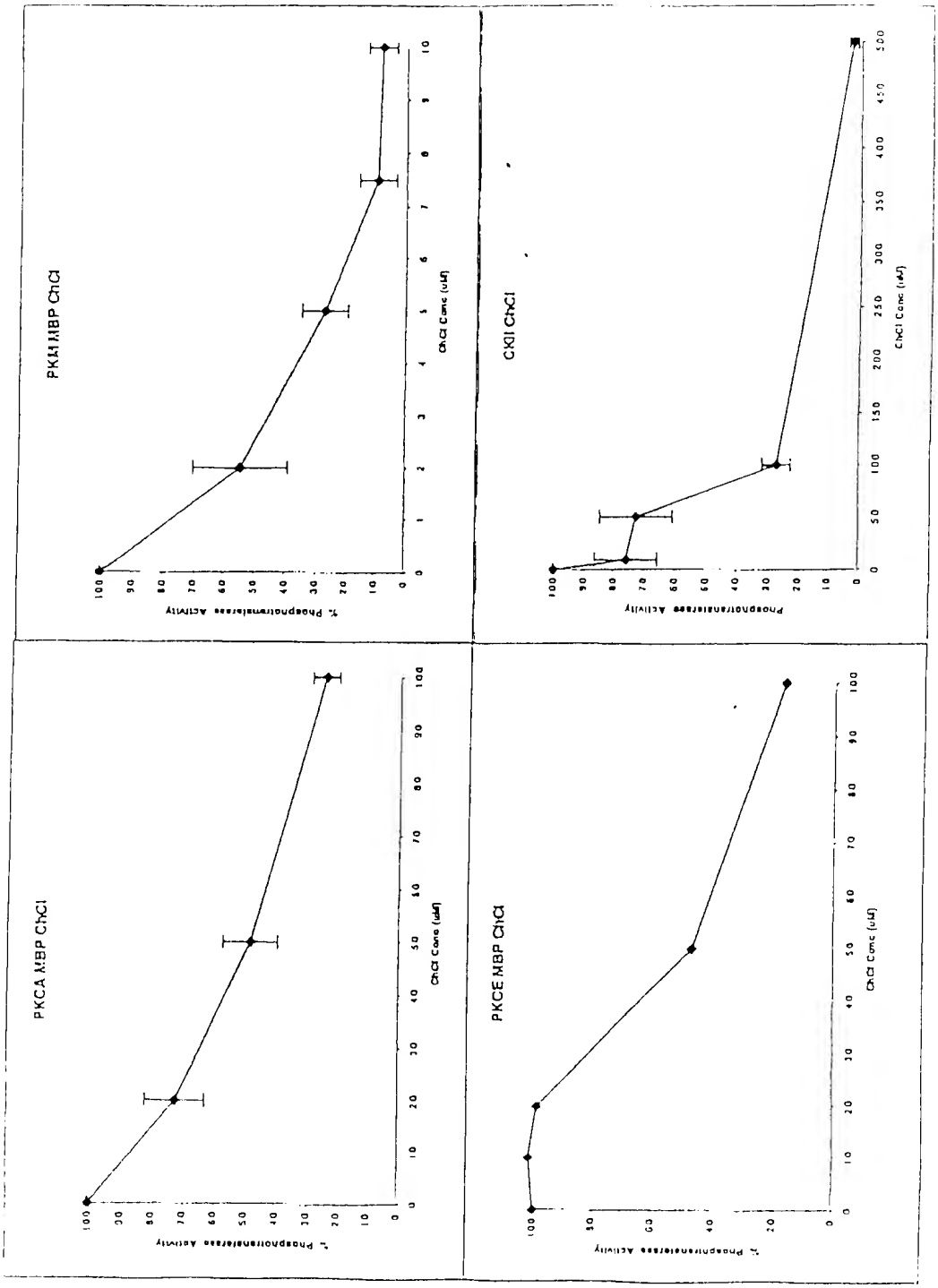
PKA MBP ChCl
% Phosphotransferase Activity
ChCl Conc (uM)
CKII ChCl
Phosphotransferase Activity
ChCl Conc (uM)
PKCA MBP ChCl
% Phosphotransferase Activity
ChCl Conc (uM)
PKCE MBP ChCl
% Phosphotransferase Activity
ChCl Conc (uM)

FIGURE 4

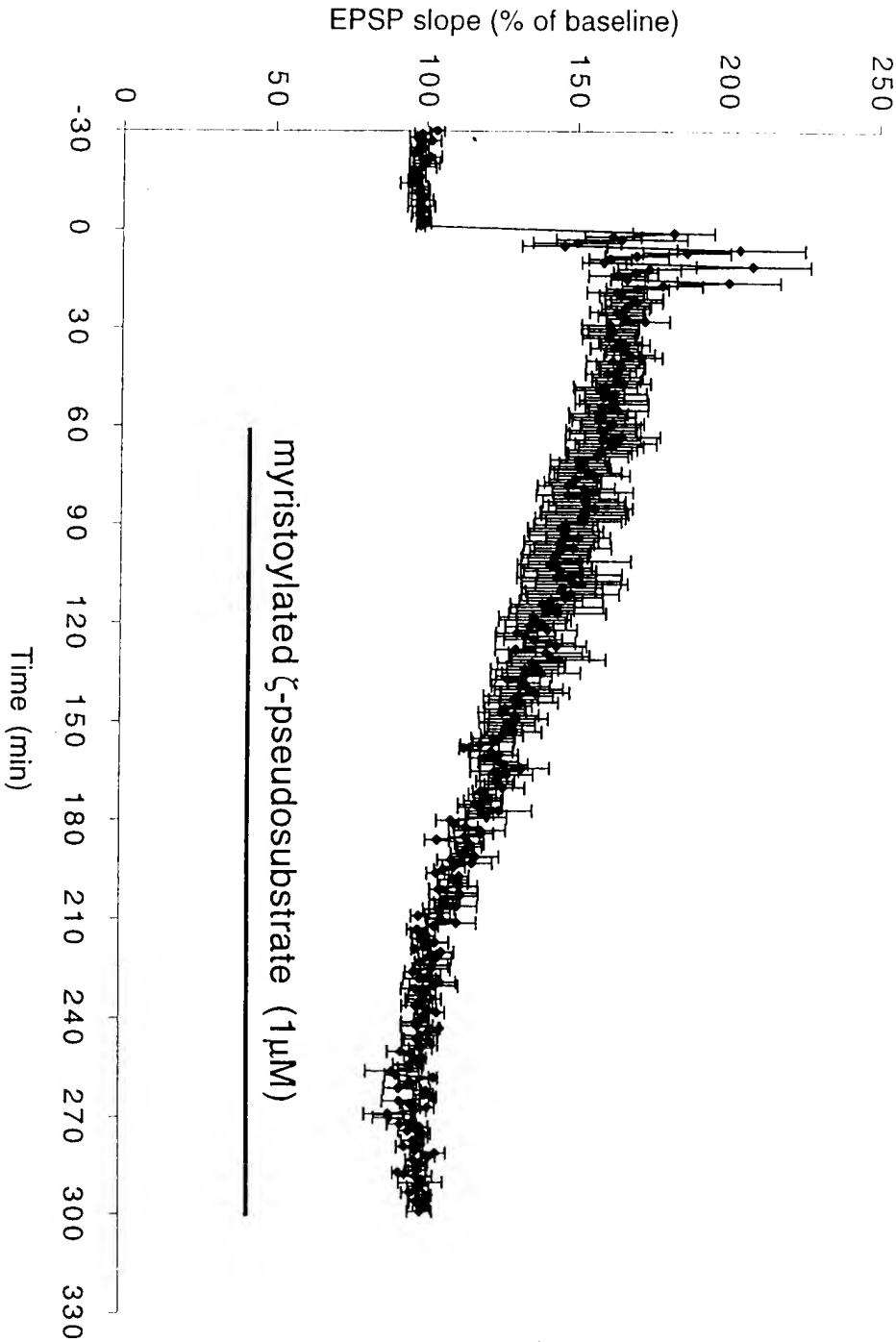

FIGURE 5

```
                10        20        30        40        50
Sense     :   CCCGGGCCTGGAGACATGAGGAGGCAGGGATGTGAGGGGCGGGGGACAGG
Antisense:   GGGCCCGGACCTCTGTACTCCTCCGTCCCTACACTCCCCGCCCCCTGTCC

                60        70        80        90       100
             ACAGCCGGCCTTCCGTTAAATATCTGCTCCTCGCGCTCGAGCCTCCCTGC
             TGTCGGCCGGAAGGCAATTTATAGACGAGGAGCGCGAGCTCGGAGGGACG

               110       120       130       140       150
             CTATTGTCGGGGCCGGAGCGAAGCCGACGCAGCATCAGCTCGTCAACGGG
             GATAACAGCCCCGGCCTCGCTTCGGCTGCGTCGTAGTCGAGCAGTTGCCC

               160       170       180       190       200
             AAGGAAGATGCCTCCCTGCACGCCCGCCGCGCACAGAGCATAAAGAATCT
             TTCCTTCTACGGAGGGACGTGCGGGCGGCGCGTGTCTCGTATTTCTTAGA

               210       220       230       240       250
             GCGCTGAGGAGGCAGGAGAAGAAAGCCGAATCTATCTACCGCCGGGGAGC
             CGCGACTCCTCCGTCCTCTTCTTTCGGCTTAGATAGATGGCGGCCCCTCG

               260       270       280       290       300
             CAGAAGATGGAGGAAGCTGTACCGTGCCAACGGCCACCTCTTCCAAGCCA
             GTCTTCTACCTCCTTCGACATGGCACGGTTGCCGGTGGAGAAGGTTCGGT

               310       320       330       340       350
             AGCGCTTTAACAGGAGAGCGTACTGCGGTCAGTGCAGCGAGAGGATATNG
             TCGCGAAATTGTCCTCTCGCATGACGCCAGTCACGTCGCTCTCCTATANC

               360       370       380       390       400
             GGCCTCGCGAGGCAAGGCTACAGGTGCATCAACTGCAAACTGCTGGTCCA
             CCGGAGCGCTCCGTTCCGATGTCCACGTAGTTGACGTTTGACGACCAGGT

               410       420       430       440       450
             TAAGCGCTGCCACGGCCTCGTCCCGCTGACCTGCAGGAAGCATATGGATT
             ATTCGCGACGGTGCCGGAGCAGGGCGACTGGACGTCCTTCGTATACCTAA
                                                      M   D>
Protein:

               460       470       480       490       500
             CTGTCATGCCTTCCCAAGAGCCTCCAGTAGACGACAAGAACGAGGACGCC
             GACAGTACGGAAGGGTTCTCGGAGGTCATCTGCTGTTCTTGCTCCTGCGG
             S   V   M   P   S   Q   E   P   P   V   D   D   K   N   E   D   A>

               510       520       530       540       550
             GACCTTCCTTCCGAGGAGACARATGGAATTGCTTACATTTCCTCATCCCG
             CTGGAAGGAAGGCTCCTCTGTYTACCTTAACGAATGTAAAGGAGTAGGGC
              D   L   P   S   E   E   T   X   G   I   A   Y   I   S   S   S   R>
```

FIGURE 6

```
       560        570        580        590        600
GAAGCATGACAGCATTAAAGACGACTCGGAGGACCTTAAGCCAGTTATCG
CTTCGTACTGTCGTAATTTCTGCTGAGCCTCCTGGAATTCGGTCAATAGC
  K  H  D  S  I  K  D  D  S  E  D  L  K  P  V  I>

       610        620        630        640        650
ATGGGATGGATGGAATCAAAATCTCTCAGGGGCTTGGGCTGCAGGACTTT
TACCCTACCTACCTTAGTTTTAGAGAGTCCCCGAACCCGACGTCCTGAAA
D  G  M  D  G  I  K  I  S  Q  G  L  G  L  Q  D  F>

       660        670        680        690        700
GACCTAATCAGAGTCATCGGGCGCGGGAGCTACGCCAAGGTTCTCCTGGT
CTGGATTAGTCTCAGTAGCCCGCGCCCTCGATGCGGTTCCAAGAGGACCA
 D  L  I  R  V  I  G  R  G  S  Y  A  K  V  L  L  V>
                  <--ATP-Binding Site---------------

       710        720        730        740        750
GCGGTTGAAGAAGAATGACCAAATTTACGCCATGAAAGTGGTGAAGAAAG
CGCCAACTTCTTCTTACTGGTTTAAATGCGGTACTTTCACCACTTCTTTC
  R  L  K  K  N  D  Q  I  Y  A  M  K  V  V  K  K>
-------------------ATP-Binding Site-------------->

       760        770        780        790        800
AGCTGGTGCATGATGACGAGGATATTGACTGGGTACAGACAGAGAAGCAC
TCGACCACGTACTACTGCTCCTATAACTGACCCATGTCTGTCTCTTCGTG
E  L  V  H  D  D  E  D  I  D  W  V  Q  T  E  K  H>

       810        820        830        840        850
GTGTTTGAGCAGGCATCCAGCAACCCCTTCCTGGTCGGATTACACTCCTG
CACAAACTCGTCCGTAGGTCGTTGGGGAAGGACCAGCCTAATGTGAGGAC
 V  F  E  Q  A  S  S  N  P  F  L  V  G  L  H  S  C>

       860        870        880        890        900
CTTCCAGACGACAAGTCGGTTGTTCCTGGTCATTGAGTACGTCAACGGCG
GAAGGTCTGCTGTTCAGCCAACAAGGACCAGTAACTCATGCAGTTGCCGC
  F  Q  T  T  S  R  L  F  L  V  I  E  Y  V  N  G>

       910        920        930        940        950
GGGACCTGATGTTCCACATGCAGAGGCAGAGGAAGCTCCCTGAGGAGCAC
CCCTGGACTACAAGGTGTACGTCTCCGTCTCCTTCGAGGGACTCCTCGTG
G  D  L  M  F  H  M  Q  R  Q  R  K  L  P  E  E  H>

       960        970        980        990       1000
GCCAGGTTCTACGCGGCCGAGATCTGCATCGCCCTCAACTTCCTGCACGA
CGGTCCAAGATGCGCCGGCTCTAGACGTAGCGGGAGTTGAAGGACGTGCT
 A  R  F  Y  A  A  E  I  C  I  A  L  N  F  L  H  E>
```

FIGURE 6 (CONT'D)

```
      1010       1020       1030       1040       1050
GAGGGGGATCATCTACAGGGACCTGAAGCTGGACAACGTCCTCCTGGATG
CTCCCCCTAGTAGATGTCCCTGGACTTCGACCTGTTGCAGGAGGACCTAC
  R  G  I  I  Y  R  D  L  K  L  D  N  V  L  L  D>

      1060       1070       1080       1090       1100
CGGACGGGCACATCAAGCTCACAGACTACGGCATGTGCAAGGAAGGCCTG
GCCTGCCCGTGTAGTTCGAGTGTCTGATGCCGTACACGTTCCTTCCGGAC
A  D  G  H  I  K  L  T  D  Y  G  M  C  K  E  G  L>

      1110       1120       1130       1140       1150
GGCCCTGGTGACACAACGAGCACTTTCTGCGGAACCCCGAATTACATCGC
CCGGGACCACTGTGTTGCTCGTGAAAGACGCCTTGGGGCTTAATGTAGCG
 G  P  G  D  T  T  S  T  F  C  G  T  P  N  Y  I  A>

      1160       1170       1180       1190       1200
CCCCGAAATCCTGCGGGGAGAGGAGTACGGGTTCAGCGTGGACTGGTGGG
GGGGCTTTAGGACGCCCCTCTCCTCATGCCCAAGTCGCACCTGACCACCC
  P  E  I  L  R  G  E  E  Y  G  F  S  V  D  W  W>

      1210       1220       1230       1240       1250
CGCTGGGAGTCCTCATGTTTGAGATGATGGCCGGGCGCTCCCCGTTCGAC
GCGACCCTCAGGAGTACAAACTCTACTACCGGCCCGCGAGGGGCAAGCTG
A  L  G  V  L  M  F  E  M  M  A  G  R  S  P  F  D>

      1260       1270       1280       1290       1300
ATCATCACCGACAACCCGGACATGAACACAGAGGACTACCTTTTCCAAGT
TAGTAGTGGCTGTTGGGCCTGTACTTGTGTCTCCTGATGGAAAAGGTTCA
 I  I  T  D  N  P  D  M  N  T  E  D  Y  L  F  Q  V>

      1310       1320       1330       1340       1350
GATCCTGGAGAAGCCCATCCGGATCCCCCGGTTCCTGTCCGTCAAAGCCT
CTAGGACCTCTTCGGGTAGGCCTAGGGGGCCAAGGACAGGCAGTTTCGGA
  I  L  E  K  P  I  R  I  P  R  F  L  S  V  K  A>

      1360       1370       1380       1390       1400
CCCATGTTTTAAAAGGATTTTTAAATAAGGACCCCAAAGAGAGGCTCGGC
GGGTACAAAATTTTCCTAAAAATTTATTCCTGGGGTTTCTCTCCGAGCCG
S  H  V  L  K  G  F  L  N  K  D  P  K  E  R  L  G>

      1410       1420       1430       1440       1450
TGCCGGCCACAGACTGGATTTTCTGACATCAAGTCCCACGCGTTCTTCCG
ACGGCCGGTGTCTGACCTAAAAGACTGTAGTTCAGGGTGCGCAAGAAGGC
 C  R  P  Q  T  G  F  S  D  I  K  S  H  A  F  F  R>
```

FIGURE 6 (CONT'D)

```
      1460       1470       1480       1490       1500
CAGCATAGACTGGGACTTGCTGGAGAAGAAGCAGGCGCTCCCTCCATTCC
GTCGTATCTGACCCTGAACGACCTCTTCTTCGTCCGCGAGGGAGGTAAGG
  S   I   D   W   D   L   L   E   K   K   Q   A   L   P   P   F>

      1510       1520       1530       1540       1550
AGCCACAGATCACAGACGACTACGGTCTGGACAACTTTGACACACAGTTC
TCGGTGTCTAGTGTCTGCTGATGCCAGACCTGTTGAAACTGTGTGTCAAG
Q   P   Q   I   T   D   D   Y   G   L   D   N   F   D   T   Q   F>

      1560       1570       1580       1590       1600
ACCAGCGAGCCCGTGCAGCTGACCCCAGACGATGAGGATGCCATAAAGAG
TGGTCGCTCGGGCACGTCGACTGGGGTCTGCTACTCCTACGGTATTTCTC
 T   S   E   P   V   Q   L   T   P   D   D   E   D   A   I   K   R>

      1610       1620       1630       1640       1650
GATCGACCAGTCAGAGTTCGAAGGCTTTGAGTATATCAACCCATTATTGC
CTAGCTGGTCAGTCTCAAGCTTCCGAAACTCATATAGTTGGGTAATAACG
  I   D   Q   S   E   F   E   G   F   E   Y   I   N   P   L   L>

      1660       1670       1680       1690       1700
TGTCCACCGAGGAGTCGGTGTGAGGCCGCGTGCGTCTCTGTCGTGGACAC
ACAGGTGGCTCCTCAGCCACACTCCGGCGCACGCAGAGACAGCACCTGTG
L   S   T   E   E   S   V>
----- C-terminus -->

      1710       1720       1730       1740       1750
GCGTGATTGACCCTTTAACTGTATCCTTAACCACCGCATATGCATGCCAG
CGCACTAACTGGGAAATTGACATAGGAATTGGTGGCGTATACGTACGGTC

      1760       1770       1780       1790       1800
GCTGGGCACGGCTCCGAGGGCGGCCAGGGACAGACGCTTGCGCCGAGACC
CGACCCGTGCCGAGGCTCCCGCCGGTCCCTGTCTGCGAACGCGGCTCTGG

      1810       1820       1830       1840       1850
GCAGAGGGAAGCGTCAGCGGGCGCTGCTGGGAGCAGAACAGTCCCTCACA
CGTCTCCCTTCGCAGTCGCCCGCGACGACCCTCGTCTTGTCAGGGAGTGT

      1860       1870       1880       1890       1900
CCTGGCCCGGCAGGCAGCTTCGTGCTGGAGGAACTTGCTGCTGTGCCTGC
GGACCGGGCCGTCCGTCGAAGCACGACCTCCTTGAACGACGACACGGACG

      1910       1920       1930       1940       1950
GTCGCGGCGGATCCGCGGGGACCCTGCCGAGGGGGCTGTCATGCGGTTTC
CAGCGCCGCCTAGGCGCCCCTGGGACGGCTCCCCCGACAGTACGCCAAAG
```

FIGURE 6 (CONT'D)

```
      1960       1970       1980       1990       2000
CAAGGTGCACATTTTCCACGGAAACAGAACTCGATGCACTGACCTGCTCC
GTTCCACGTGTAAAAGGTGCCTTTGTCTTGAGCTACGTGACTGGACGAGG

      2010       2020       2030       2040       2050
GCCAGGAAAGTGAGCGTGTAGCGTCCTGAGGAATAAAATGTTCCGATGAA
CGGTCCTTTCACTCGCACATCGCAGGACTCCTTATTTTACAAGGCTACTT

AAAAAAAA
TTTTTTTT
```

FIGURE 6 (CONT'D)

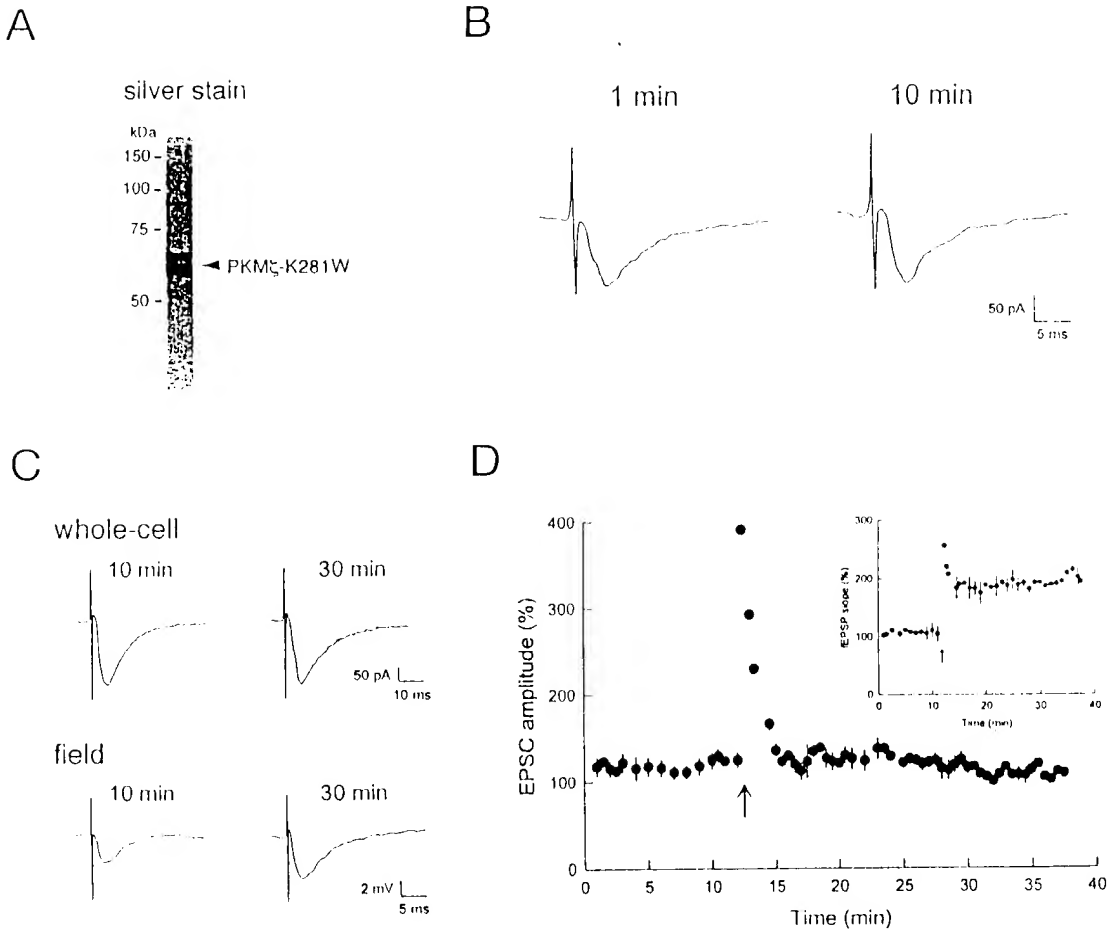
A
silver stain
kDa
150
100
75
50
PKMζ-K281W
B
1 min
10 min
50 pA
5 ms
C
whole-cell
10 min
30 min
50 pA
10 ms
field
10 min
30 min
2 mV
5 ms
D
EPSC amplitude (%)
Time (min)

FIGURE 7